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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/783,931

DATE: 12/05/2001
TIME: 11:51:31

Input Set : A:\7326-122
Output Set: N:\CRF3\11212001\I783931.raw

ENTERED

SEQUENCE LISTING

C--> 5 (1) GENERAL INFORMATION:
7 (i) APPLICANT: Ish-Horowicz, David
8 Henrique, Domingos Manuel Pinto
9 Lewis, Julian Hart
10 Artavanis-Tsakonas, Spyridon
11 Gray, Grace
C--> 13 (ii) TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
14 AND FRAGMENTS
16 (iii) NUMBER OF SEQUENCES: 94
18 (iv) CORRESPONDENCE ADDRESS:
19 (A) ADDRESSEE: Pennie & Edmonds LLP
20 (B) STREET: 1155 Avenue of the Americas
21 (C) CITY: New York
22 (D) STATE: NY
23 (E) COUNTRY: USA
24 (F) ZIP: 10036/2711
26 (v) COMPUTER READABLE FORM:
27 (A) MEDIUM TYPE: Diskette
28 (B) COMPUTER: IBM Compatible
29 (C) OPERATING SYSTEM: DOS
30 (D) SOFTWARE: FastSEQ Version 2.0
32 (vi) CURRENT APPLICATION DATA:
33 (A) APPLICATION NUMBER: US/09/783,931
C--> 34 (B) FILING DATE: 15-Feb-2001
40 (C) CLASSIFICATION:
37 (vii) PRIOR APPLICATION DATA:
38 (A) APPLICATION NUMBER: 08/981,392
39 (B) FILING DATE: 22-DEC-1997
42 (viii) ATTORNEY/AGENT INFORMATION:
43 (A) NAME: Antler, Adriane M.
44 (B) REGISTRATION NUMBER: 32,605
45 (C) REFERENCE/DOCKET NUMBER: 7326-122
47 (ix) TELECOMMUNICATION INFORMATION:
48 (A) TELEPHONE: 212-790-9090
49 (B) TELEFAX: 212-869-8864
50 (C) TELEX: 66141 PENNIE
53 (2) INFORMATION FOR SEQ ID NO: 1:
55 (i) SEQUENCE CHARACTERISTICS:
56 (A) LENGTH: 2508 base pairs
57 (B) TYPE: nucleic acid
58 (C) STRANDEDNESS: single
59 (D) TOPOLOGY: linear
W--> 61 (ii) MOLECULE TYPE: DNA
62 (ix) FEATURE:
64 (A) NAME/KEY: Coding Sequence
65 (B) LOCATION: 277...2460

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(D) OTHER INFORMATION:

66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 69 GAATTCGGCA CGAGGTTTT TTTTTTTTT TTCCCTCTT TTCTTTCTT TCCTTTGCC 60
 71 ATCCGAAAGA GCTGTCAGCC GCCGCCGGGC TGCACCTAA GGCCTCGGTAA GGGGGATAAC 120
 72 AGTCAGAGAC CCTCCTGAAA GCAGGAGACG GGACGGTACC CCTCCGGCTC TGCGGGCGG 180
 73 CTGCGGCCCG TCCGTTCTTT CCCCTCCCC GAGAGACACT CTTCCCTTCC CCCCCACGAAG 240
 74 ACACAGGGGC AGGAACGCGA GCGCTGCCCT TCCGCC ATG GGA GGC CGC TTC CTG 294
 75 Met Gly Gly Arg Phe Leu
 76 1 5
 77 CTG ACG CTC GCC CTC CTC TCG GCG CTG CTG CGC TGC CAG GTT GAC 342
 79 Leu Thr Leu Ala Leu Leu Ser Ala Leu Leu Cys Arg Cys Gln Val Asp
 80 10 15 20
 81 GGC TCC GGG GTG TTC GAG CTG AAG CTG CAG GAG TTT GTC AAC AAG AAG 390
 83 Gly Ser Gly Val Phe Glu Leu Lys Leu Gln Glu Phe Val Asn Lys Lys
 84 25 30 35
 85 GGG CTG CTC AGC AAC CGC AAC TGC TGC CGG GGG GGC GGC CCC GGA GGC 438
 87 Gly Leu Leu Ser Asn Arg Asn Cys Cys Arg Gly Gly Pro Gly Gly
 88 40 45 50
 89 GCC GGG CAG CAG CAG TGC GAC TGC AAG ACC TTC TTC CGC GTC TGC CTG 486
 91 Ala Gly Gln Gln Gln Cys Asp Cys Lys Thr Phe Phe Arg Val Cys Leu
 92 55 60 65 70
 93 AAG CAC TAC CAG GCC AGC GTC TCC CCC GAG CCG CCC TGC ACC TAC GGC 534
 95 Lys His Tyr Gln Ala Ser Val Ser Pro Glu Pro Pro Cys Thr Tyr Gly
 96 75 80 85
 97 AGC GCC ATC ACC CCC GTC CTC GGC GCC AAC TCC TTC AGC GTC CCC GAC 582
 99 Ser Ala Ile Thr Pro Val Leu Gly Ala Asn Ser Phe Ser Val Pro Asp
 100 90 95 100
 101 GGC GCG GGC GGC GAC CCC GCC TTC AGC AAC CCC ATC CGC TTC CCC 630
 103 Gly Ala Gly Ala Asp Pro Ala Phe Ser Asn Pro Ile Arg Phe Pro
 104 105 110 115
 105 TTC GGC TTC ACC TGG CCC GGC ACC TTC TCG CTC ATC ATC GAG GCT CTG 678
 107 Phe Gly Phe Thr Trp Pro Gly Thr Phe Ser Leu Ile Ile Glu Ala Leu
 108 120 125 130
 109 CAC ACC GAC TCC CCC GAC CTC ACC ACA GAA AAC CCC GAG CGC CTC 726
 111 His Thr Asp Ser Pro Asp Asp Leu Thr Thr Glu Asn Pro Glu Arg Leu
 112 135 140 145 150
 113 ATC AGC CGC CTG GCC ACC CAG AGG CAC CTG GCG GTG GGC GAG GAG TGG 774
 115 Ile Ser Arg Leu Ala Thr Gln Arg His Leu Ala Val Gly Glu Trp
 116 155 160 165
 117 TCC CAG GAC CTG CAC AGC AGC GGC CGC ACC GAC CTC AAG TAC TCC TAT 822
 119 Ser Gln Asp Leu His Ser Ser Gly Arg Thr Asp Leu Lys Tyr Ser Tyr
 120 170 175 180
 121 CGC TTT GTG TGT GAT GAG CAC TAC TAC GGG GAA GGC TGC TCT GTC TTC 870
 123 Arg Phe Val Cys Asp Glu His Tyr Tyr Gly Glu Gly Cys Ser Val Phe
 124 185 190 195
 125 TGC CGG CCC CGT GAC GAC CGC TTC GGT CAC TTC ACC TGT GGA GAG CGT 918
 127 Cys Arg Pro Arg Asp Asp Arg Phe Gly His Phe Thr Cys Gly Glu Arg
 128 200 205 210
 129 GGC GAG AAG GTC TGC AAC CCA GGC TGG AAG GGC CAG TAC TGC ACT GAG 966
 131

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132	Gly Glu Lys Val Cys Asn Pro Gly Trp Lys Gly Gln Tyr Cys Thr Glu			
133	215	220	225	230
135	CCG ATT TGC TTG CCT GGG TGT GAC GAG CAG CAC GGC TTC TGC GAC AAA			1014
136	Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln His Gly Phe Cys Asp Lys			
137	235	240	245	
139	CCT GGG GAA TGC AAG TGC AGA GTG GGT TGG CAG GGG CGG TAC TGT GAC			
140	Pro Gly Glu Cys Lys Cys Arg Val Gly Trp Gln Gly Arg Tyr Cys Asp			
141	250	255	260	
143	GAG TGC ATC CGA TAC CCA GGC TGC CTG CAC GGT ACC TGT CAG CAG CCA			
144	Glu Cys Ile Arg Tyr Pro Gly Cys Leu His Gly Thr Cys Gln Gln Pro			
145	265	270	275	
147	TGG CAG TGC AAC TGC CAG GAA GGC TGG GGC GGC CTT TTC TGC AAC CAG			1158
148	Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly Gly Leu Phe Cys Asn Gln			
149	280	285	290	
151	GAC CTG AAC TAC TGC ACT CAC CAC AAG CCA TGC AAG AAT GGT GCC ACA			
152	Asp Leu Asn Tyr Cys Thr His His Lys Pro Cys Lys Asn Gly Ala Thr			
153	295	300	305	310
155	TGC ACC AAC ACC GGT CAG GGG AGC TAC ACT TGT TCT TGC CGA CCT GGG			
156	Cys Thr Asn Thr Gly Gln Gly Ser Tyr Thr Cys Ser Cys Arg Pro Gly			
157	315	320	325	
159	TAC ACA GGC TCC AGC TGC GAG ATT GAA ATC AAC GAA TGT GAT GCC AAC			
160	Tyr Thr Gly Ser Ser Cys Glu Ile Glu Ile Asn Glu Cys Asp Ala Asn			
161	330	335	340	
163	CCT TGC AAG AAT GGT GGA AGC TGC ACG GAT CTC GAG AAC AGC TAT TCC			1350
164	Pro Cys Lys Asn Gly Gly Ser Cys Thr Asp Leu Glu Asn Ser Tyr Ser			
165	345	350	355	
167	TGT ACC TGC CCC CCA GGC TTC TAT GGT AAA AAC TGT GAG CTG AGT GCA			1398
168	Cys Thr Cys Pro Pro Gly Phe Tyr Gly Lys Asn Cys Glu Leu Ser Ala			
169	360	365	370	
171	ATG ACT TGT GCT GAT GGA CCG TGC TTC AAT GGA GGG CGA TGC ACT GAC			
172	Met Thr Cys Ala Asp Gly Pro Cys Phe Asn Gly Gly Arg Cys Thr Asp			
173	375	380	385	390
175	AAC CCT GAT GGT GGA TAC AGC TGC CGC TGC CCA CTG GGT TAT TCT GGG			
176	Asn Pro Asp Gly Gly Tyr Ser Cys Arg Cys Pro Leu Gly Tyr Ser Gly			
177	395	400	405	
179	TTC AAC TGT GAA AAG AAA ATC GAT TAC TGC AGT TCC AGC CCT TGT GCT			1446
180	Phe Asn Cys Glu Lys Ile Asp Tyr Cys Ser Ser Pro Cys Ala			
181	410	415	420	
183	AAT GGA GCC CAG TGC GTT GAC CTG GGG AAC TCC TAC ATA TGC CAG TGC			1590
184	Asn Gly Ala Gln Cys Val Asp Leu Gly Asn Ser Tyr Ile Cys Gln Cys			
185	425	430	435	
187	CAG GCT GGC TTC ACT GGC AGG CAC TGT GAC GAC AAC GTG GAC GAT TGC			1638
188	Gln Ala Gly Phe Thr Gly Arg His Cys Asp Asp Asn Val Asp Asp Cys			
189	440	445	450	
191	GCC TCC TTC CCC TGC GTC AAT GGA GGG ACC TGT CAG GAT GGG GTC AAC			1686
192	Ala Ser Phe Pro Cys Val Asn Gly Gly Thr Cys Gln Asp Gly Val Asn			
193	455	460	465	470
195	GAC TAC TCC TGC ACC TGC CCC CCG GGA TAC AAC GGG AAG AAC TGC AGC			
196	Asp Tyr Ser Cys Thr Cys Pro Pro Gly Tyr Asn Gly Lys Asn Cys Ser			

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197	475	480	485		
199	ACG CCG GTG AGC AGA TGC GAG CAC AAC CCC TGC CAC AAT GGG GCC ACC			1782	
200	Thr Pro Val Ser Arg Cys Glu His Asn Pro Cys His Asn Gly Ala Thr				
201	490	495	500		
203	TGC CAC GAG AGA AGC AAC CGC TAC GTG TGC GAG TGC GCT CGG GGC TAC			1830	
204	Cys His Glu Arg Ser Asn Arg Tyr Val Cys Glu Cys Ala Arg Gly Tyr				
205	505	510	515		
207	GGC GGC CTC AAC TGC CAG TTC CTG CTC CCC GAG CCA CCT CAG GGG CCG			1878	
208	Gly Gly Leu Asn Cys Gln Phe Leu Leu Pro Glu Pro Pro Gln Gly Pro				
209	520	525	530		
211	GTC ATC GTT GAC TTC ACC GAG AAG TAC ACA GAG GGC CAG AAC AGC CAG			1926	
212	Val Ile Val Asp Phe Thr Glu Lys Tyr Thr Glu Gly Gln Asn Ser Gln				
213	535	540	545	550	
215	TTT CCC TGG ATC GCA GTG TGC GCC GGG ATT ATT CTG GTC CTC ATG CTG			1974	
216	Phe Pro Trp Ile Ala Val Cys Ala Gly Ile Ile Leu Val Leu Met Leu				
217	555	560	565		
219	CTG CTG GGT TGC GCC GCC ATC GTC GTC TGC GTC AGG CTG AAG GTG CAG			2022	
220	Leu Leu Gly Cys Ala Ala Ile Val Val Cys Val Arg Leu Lys Val Gln				
221	570	575	580		
223	AAG AGG CAC CAC CAG CCC GAG GCC TGC AGG AGT GAA ACG GAG ACC ATG			2070	
224	Lys Arg His His Gln Pro Glu Ala Cys Arg Ser Glu Thr Glu Thr Met				
225	585	590	595		
227	AAC AAC CTG GCG AAC TGC CAG CGC GAG AAG GAC ATC TCC ATC AGC GTC			2118	
228	Asn Asn Leu Ala Asn Cys Gln Arg Glu Lys Asp Ile Ser Ile Ser Val				
229	600	605	610		
231	ATC GGT GCC ACT CAG ATT AAA AAC ACA AAT AAG AAA GTA GAC TTT CAC			2166	
232	Ile Gly Ala Thr Gln Ile Lys Asn Thr Asn Lys Lys Val Asp Phe His				
233	615	620	625	630	
235	AGC GAT AAC TCC GAT AAA AAC GGC TAC AAA GTT AGA TAC CCA TCA GTG			2214	
236	Ser Asp Asn Ser Asp Lys Asn Gly Tyr Lys Val Arg Tyr Pro Ser Val				
237	635	640	645		
239	GAT TAC AAT TTG GTG CAT GAA CTC AAG AAT GAG GAC TCT GTG AAA GAG			2262	
240	Asp Tyr Asn Leu Val His Glu Leu Lys Asn Glu Asp Ser Val Lys Glu				
241	650	655	660		
243	GAG CAT GGC AAA TGC GAA GCC AAG TGT GAA ACG TAT GAT TCA GAG GCA			2310	
244	Glu His Gly Lys Cys Glu Ala Lys Cys Glu Thr Tyr Asp Ser Glu Ala				
245	665	670	675		
247	GAA GAG AAA AGC GCA GTA CAG CTA AAA AGT AGT GAC ACT TCT GAA AGA			2358	
248	Glu Glu Lys Ser Ala Val Gln Leu Lys Ser Ser Asp Thr Ser Glu Arg				
249	680	685	690		
251	AAA CGG CCA GAT TCA GTA TAT TCC ACT TCA AAG GAC ACA AAG TAC CAG			2406	
252	Lys Arg Pro Asp Ser Val Tyr Ser Thr Ser Lys Asp Thr Lys Tyr Gln				
253	695	700	705	710	
255	TCG GTG TAC GTC ATA TCA GAA GAG AAA GAT GAG TGC ATC ATA GCA ACT			2454	
256	Ser Val Tyr Val Ile Ser Glu Glu Lys Asp Glu Cys Ile Ile Ala Thr				
257	715	720	725		
259	GAG GTG TAAAACAGAC GTGACGTGGC AAAGCTTATC GATACCGTCA TCAAGCTT			2508	
260	Glu Val				
264	(2) INFORMATION FOR SEQ ID NO: 2:				

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266 (i) SEQUENCE CHARACTERISTICS:
267 (A) LENGTH: 728 amino acids
268 (B) TYPE: amino acid
269 (C) STRANDEDNESS:
270 (D) TOPOLOGY: unknown
272 (ii) MOLECULE TYPE: protein

274 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
276 Met Gly Arg Phe Leu Leu Thr Leu Ala Leu Leu Ser Ala Leu Leu
277 1 5 10 15
278 Cys Arg Cys Gln Val Asp Gly Ser Gly Val Phe Glu Leu Lys Leu Gln
279 20 25 30
280 Glu Phe Val Asn Lys Lys Gly Leu Leu Ser Asn Arg Asn Cys Cys Arg
281 35 40 45
282 Gly Gly Gly Pro Gly Gly Ala Gly Gln Gln Cys Asp Cys Lys Thr
283 50 55 60
284 Phe Phe Arg Val Cys Leu Lys His Tyr Gln Ala Ser Val Ser Pro Glu
285 65 70 75 80
286 Pro Pro Cys Thr Tyr Gly Ser Ala Ile Thr Pro Val Leu Gly Ala Asn
287 85 90 95
288 Ser Phe Ser Val Pro Asp Gly Ala Gly Gly Ala Asp Pro Ala Phe Ser
289 100 105 110
290 Asn Pro Ile Arg Phe Pro Phe Gly Phe Thr Trp Pro Gly Thr Phe Ser
291 115 120 125
292 Leu Ile Ile Glu Ala Leu His Thr Asp Ser Pro Asp Asp Leu Thr Thr
293 130 135 140
294 Glu Asn Pro Glu Arg Leu Ile Ser Arg Leu Ala Thr Gln Arg His Leu
295 145 150 155 160
296 Ala Val Gly Glu Glu Trp Ser Gln Asp Leu His Ser Ser Gly Arg Thr
297 165 170 175
298 Asp Leu Lys Tyr Ser Tyr Arg Phe Val Cys Asp Glu His Tyr Tyr Gly
299 180 185 190
300 Glu Gly Cys Ser Val Phe Cys Arg Pro Arg Asp Asp Arg Phe Gly His
301 195 200 205
302 Phe Thr Cys Gly Glu Arg Gly Glu Lys Val Cys Asn Pro Gly Trp Lys
303 210 215 220
304 Gly Gln Tyr Cys Thr Glu Pro Ile Cys Leu Pro Gly Cys Asp Glu Gln
305 225 230 235 240
306 His Gly Phe Cys Asp Lys Pro Gly Glu Cys Lys Cys Arg Val Gly Trp
307 245 250 255
308 Gln Gly Arg Tyr Cys Asp Glu Cys Ile Arg Tyr Pro Gly Cys Leu His
309 260 265 270
310 Gly Thr Cys Gln Gln Pro Trp Gln Cys Asn Cys Gln Glu Gly Trp Gly
311 275 280 285
312 Gly Leu Phe Cys Asn Gln Asp Leu Asn Tyr Cys Thr His His Lys Pro
313 290 295 300
314 Cys Lys Asn Gly Ala Thr Cys Thr Asn Thr Gly Gln Gly Ser Tyr Thr
315 305 310 315 320
316 Cys Ser Cys Arg Pro Gly Tyr Thr Gly Ser Ser Cys Glu Ile Glu Ile
317 325 330 335

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/783,931

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Input Set : A:\7326-122
Output Set: N:\CRF3\11212001\I783931.raw

L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
 L:13 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
 L:33 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
 L:34 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
 L:61 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
 L:377 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
 L:439 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4
 L:798 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
 L:1204 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=14
 L:1201 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
 L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:1243 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
 L:1245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
 L:1266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:1295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
 L:1301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
 L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
 L:1328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
 L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
 L:1404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
 L:1406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
 L:1414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
 L:1433 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
 L:1510 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
 L:1665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
 L:1684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
 L:1721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
 L:1723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
 L:1746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
 L:1765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
 L:1767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
 L:1812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
 L:1816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
 L:1818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
 L:1833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
 L:1848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
 L:1891 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
 L:1943 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
 L:1964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
 L:1966 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
 L:1968 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
 L:1972 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
 L:1974 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
 L:1980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
 L:1982 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
 L:1997 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
 L:2075 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
 L:2094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52

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L:2096 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52
L:2228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
L:2251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
L:2268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:2270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:2272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62
L:2276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:2295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:2297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:2314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:2316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
L:2611 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=81
L:2645 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=82
L:2723 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=86
L:2762 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=87
L:2807 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=89
L:2852 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=91
L:2897 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=93